

Exhibit B



Conserved Domain Database

1/2

PubMed

Nucleotide

Protein

Structure

CDD

Taxonomy

Help?

CD: pfam02877.8_PARP_reg

PSSM-Id: 3371

Source: Pfam[US], Pfam[UK]

Description: Poly(ADP-ribose) polymerase, regulatory domain. Poly(ADP-ribose) polymerase catalyses the covalent attachment of ADP-ribose units from NAD⁺ to itself and to a limited number of other DNA binding proteins, which decreases their affinity for DNA. Poly(ADP-ribose) polymerase is a regulatory component induced by DNA damage. The carboxyl-terminal region is the most highly conserved region of the protein. Experiments have shown that a carboxyl 40 kDa fragment is still catalytically active.

Taxa: Eukaryota

References: 3 PubMed Links

Status: Alignment from source

Created: 11-Apr-2003

Aligned: 6 rows

PSSM: 134 columns

Representative: Consensus

Proteins: [\[Click here for CDART summary of Proteins containing pfam02877\]](#)

View 3D Structure

with Cn3D

using Virtual Bonds

(To display structure, download [Cn3D](#))

View Alignment

as Hypertext

width 60

color at 2.0 bits

Subset Rows

up to 10

of the most diverse members

```

      10      20      30      40      50      60
consensus  ....*.....*.....*.....*.....*.....*.....*.....
3PAX       1  HSKLLKSVQDLINLIFDVDSMAQTMEFEI--DMEIMPLGKLSFRQIQSAYRVLEIYEV  58
gi_1353140 171  LLNQLK-FNEAFGRPIDCLSLAQLTTCYEIIsKIEEGTGGKQARRSTGRGFFVADPVLAV  229
gi_1709740 206  QSNLDTAVAKTISLICHVSMKAQHMEIGY--NANLLELAGTISKSTISRGYEVLEKRISEV  243
gi_548585   644  TQKLETSVQNLINLITDIDGSHNKTLMFEFHI--DMDEMPLGKLSAQIQSAYRVVNEIYNV  701
gi_1709741 647  RSKFLPLSVQDLINLIMFDVDSMERTMMEFDL--DMEIMPLGKLSQFQIQSAYFVLEIYEL  704

      70      80      90     100     110     120
consensus  ....*.....*.....*.....*.....*.....*.....*.....
3PAX       59  IGDGGSEAKLIDLSNRFYTLIPHDFGFKRPP--LIETHQKIQAQRQMLDALK-EIEVAYS  115
gi_1353140 270  VDDGGSESQLLDLSNRFYTLIPHDFGMMNFF--LLSHLEYIQAKVQMLDNL-DIEVAYS  123
gi_1709740 344  RDCGFS---LRDI-NKYISLIPHSFGFCVPP--KIDSHAKTQAERELLDALKgSIEASLE  283
gi_548585   344  I-DFYDRTPLBELGGEFYTVIPHDFGFMHQCqFVIDTPQHLKQNIEMVEALG-EIELATK  401
gi_1709741 702  LEQGSNTAKLIIDATNRFYTLIPHNFGVQLPT--LIETHQQIEELPQMLDLSLA-EIEVAYS  756
gi_1709741 708  IQGGSTNAKFIIDATNRFYTLIPHNFGTQSPF--LLDTTEQVEQLRQMLDGLI-EIECAYS  761

      130
consensus  ....*.....*.....
3PAX      116  LLDLERTASDKDELDPEHYE  124
gi_1353140 284  LFDLFTTASSFNDIYQRLYE  302
gi_1709740 402  LLSVDPLGLQD-DELTTHYQ  419
gi_548585   769  IIKSEIVSDACNPLDNHYA  777
gi_1709741 762  LLQTEISKADINPEIDKHYE  780
```

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